Serial No. 09/147,405

IN THE SPECIFICATION:

Please replace the paragraph beginning on page 9, line 24, and ending on page 10, line 5, with the following replacement paragraph:
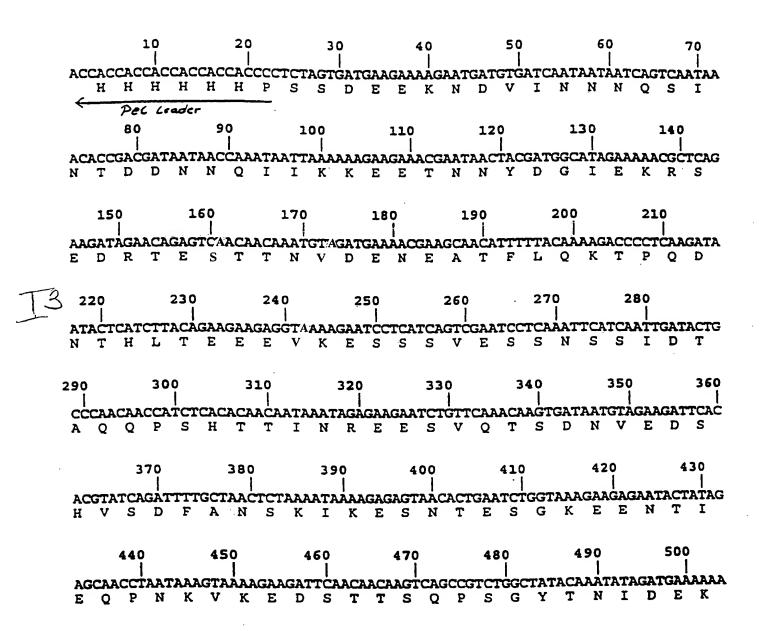
--Example 3: DNA sequencing and sequence analysis

Eight colonies coming from the second panning (pH 3.4) against fibrinogen described in Example 2 were chosen for further studies. Phagemid DNA from these colonies was prepared and partially sequenced. Seven of the clones seemed to contain the same insert. One of these seven clones called pSE100 was chosen for further studies. Purified phagemid DNA from the clone pSE100 was analysed by restriction mapping which revealed that the phagemid contained an insert of ~ 1.8 kilo base pair (kb). The nucleotide (nt) sequences of the complete inserts of pSE100 were determined and the nt and deduced amino acid (aa) sequences were analysed using the PC-gene program. This analysis revealed that the insert of pSE100 contains an open reading frame of 1.745 nt (sequence list). Thus the insert encodes a 582 aa protein, termed protein FIG (and the corresponding gene termed *fig*), with a calculated molecular mass of -65 kDa (sequence list). Furthermore, the sequence analysis show that the insert of pSE100 is in the correct reading frame with the vector sequences in the 5'-and 3'-ends. This means that the insert gives rise to a fusion with the *pel* leader and the *myc* tail (sequence list) and that he native 5'- and 3'-ends of the *fig* gene is not present in the pSE100 clone.--

Please replace the paragraph beginning with the term "**Sequence list**" on page 19, line 1 and ending with the last line of text on page 21, with the following replacement paragraph:

**Sequence list** (SEQ ID NO: 10)

```
          10        20        30        40        50        60        70
          |         |         |         |         |         |         |
ACCACCACCACCACCACCACCCCCTCTAGTGATGAAGAAAAGAATGATGTGATCAATAATAATCAGTCAATAA
    H  H  H  H  H  H  P  S  S  D  E  E  K  N  D  V  I  N  N  N  Q  S  I
```
←— Pel Leader

```
          80        90        100       110       120       130       140
          |         |         |         |         |         |         |
ACACCGACGATAATAACCAAATAATTAAAAAAGAAGAAACGAATAACTACGATGGCATAGAAAAACGCTCAG
  N  T  D  D  N  N  Q  I  I  K  K  E  E  T  N  N  Y  D  G  I  E  K  R  S
```

```
          150       160       170       180       190       200       210
          |         |         |         |         |         |         |
AAGATAGAACAGAGTCAACAACAAATGTAGATGAAAACGAAGCAACATTTTTACAAAAGACCCCTCAAGATA
  E  D  R  T  E  S  T  T  N  V  D  E  N  E  A  T  F  L  Q  K  T  P  Q  D
```

I3

```
          220       230       240       250       260       270       280
          |         |         |         |         |         |         |
ATACTCATCTTACAGAAGAAGAGGTAAAAGAATCCTCATCAGTCGAATCCTCAAATTCATCAATTGATACTG
  N  T  H  L  T  E  E  E  V  K  E  S  S  S  V  E  S  S  N  S  S  I  D  T
```

```
  290       300       310       320       330       340       350       360
  |         |         |         |         |         |         |         |
CCCAACAACCATCTCACACAACAATAAATAGAGAAGAATCTGTTCAAACAAGTGATAATGTAGAAGATTCAC
  A  Q  Q  P  S  H  T  T  I  N  R  E  E  S  V  Q  T  S  D  N  V  E  D  S
```

```
          370       380       390       400       410       420       430
          |         |         |         |         |         |         |
ACGTATCAGATTTTGCTAACTCTAAAATAAAAGAGAGTAACACTGAATCTGGTAAAGAAGAGAATACTATAG
  H  V  S  D  F  A  N  S  K  I  K  E  S  N  T  E  S  G  K  E  E  N  T  I
```

```
          440       450       460       470       480       490       500
          |         |         |         |         |         |         |
AGCAACCTAATAAAGTAAAAGAAGATTCAACAACAAGTCAGCCGTCTGGCTATACAAATATAGATGAAAAAA
  E  Q  P  N  K  V  K  E  D  S  T  T  S  Q  P  S  G  Y  T  N  I  D  E  K
```

```
        510           520           530           540           550           560           570
         |             |             |             |             |             |             |
TTTCAAATCAAGATGAGTTATTAAATTTACCAATAAATGAATATGAAAATAAGGCTAGACCATTATCTACAA
 I  S  N  Q  D  E  L  L  N  L  P  I  N  E  Y  E  N  K  A  R  P  L  S  T

        580           590           600           610           620           630           640
         |             |             |             |             |             |             |
CATCTGCCCAACCATCGATTAAACGTGTAACCGTAAATCAATTAGCGGCGGAACAAGGTTCGAATGTTAACC
 T  S  A  Q  P  S  I  K  R  V  T  V  N  Q  L  A  A  E  Q  G  S  N  V  N

        650           660           670           680           690           700           710           720
         |             |             |             |             |             |             |             |
ATTTAATTAAAGTTACTGATCAAAGTATTACTGAAGGATATGATGATAGTGAAGGTGTTATTAAAGCACATG
 H  L  I  K  V  T  D  Q  S  I  T  E  G  Y  D  D  S  E  G  V  I  K  A  H

        730           740           750           760           770           780           790
         |             |             |             |             |             |             |
ATGCTGAAAACTTAATCTATGATGTAACTTTTGAAGTAGATGATAAGGTGAAATCTGGTGATACGATGACAG
 D  A  E  N  L  I  Y  D  V  T  F  E  V  D  D  K  V  K  S  G  D  T  M  T

        800           810           820           830           840           850           860
         |             |             |             |             |             |             |
TGGATATAGATAAGAATACAGTTCCATCAGATTTAACCGATAGCTTTACAATACCAAAAATAAAAGATAATT
 V  D  I  D  K  N  T  V  P  S  D  L  T  D  S  F  T  I  P  K  I  K  D  N

        870           880           890           900           910           920           930
         |             |             |             |             |             |             |
CTGGAGAAATCATCGCTACAGGTACTTATGATAACAAAAATAAACAAATCACCTATACTTTTACAGATTATG
 S  G  E  I  I  A  T  G  T  Y  D  N  K  N  K  Q  I  T  Y  T  F  T  D  Y

        940           950           960           970           980           990           1000
         |             |             |             |             |             |             |
TAGATAAGTATGAAAATATTAAAGCACACCTTAAATTAACGTCATACATTGATAAATCAAAGGTTCCAAATA
 V  D  K  Y  E  N  I  K  A  H  L  K  L  T  S  Y  I  D  K  S  K  V  P  N

       1010          1020          1030          1040          1050          1060          1070          1080
         |             |             |             |             |             |             |             |
ATAATACCAAGTTAGATGTAGAATATAAAACGGCCCTTTCATCAGTAAATAAAACAATTACGGTTGAATATC
 N  N  T  K  L  D  V  E  Y  K  T  A  L  S  S  V  N  K  T  I  T  V  E  Y

       1090          1100          1110          1120          1130          1140          1150
         |             |             |             |             |             |             |
AAAGACCTAACGAAAATCGGACTGCTAACCTTCAAAGTATGTTTACAAATATAGATACGAAAAATCATACAG
 Q  R  P  N  E  N  R  T  A  N  L  Q  S  M  F  T  N  I  D  T  K  N  H  T

       1160          1170          1180          1190          1200          1210          1220
         |             |             |             |             |             |             |
TTGAGCAAACGATTTATATTAACCCTCTTCGTTATTCAGCCAAGGAAACAAATGTAAATATTTCAGGGAATG
 V  E  Q  T  I  Y  I  N  P  L  R  Y  S  A  K  E  T  N  V  N  I  S  G  N
```
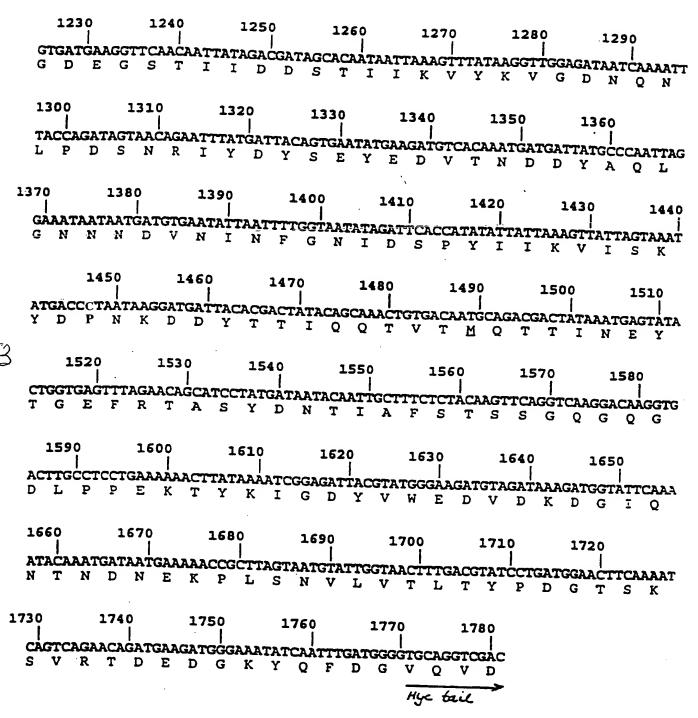
```
        1230            1240            1250            1260            1270            1280            1290
          |               |               |               |               |               |               |
GTGATGAAGGTTCAACAATTATAGACGATAGCACAATAATTAAAGTTTATAAGGTTGGAGATAATCAAAATT
  G   D   E   G   S   T   I   I   D   D   S   T   I   I   K   V   Y   K   V   G   D   N   Q   N

        1300            1310            1320            1330            1340            1350            1360
          |               |               |               |               |               |               |
TACCAGATAGTAACAGAATTTATGATTACAGTGAATATGAAGATGTCACAAATGATGATTATGCCCAATTAG
  L   P   D   S   N   R   I   Y   D   Y   S   E   Y   E   D   V   T   N   D   D   Y   A   Q   L

      1370            1380            1390            1400            1410            1420            1430            1440
        |               |               |               |               |               |               |               |
GAAATAATAATGATGTGAATATTAATTTTGGTAATATAGATTCACCATATATTATTAAAGTTATTAGTAAAT
  G   N   N   N   D   V   N   I   N   F   G   N   I   D   S   P   Y   I   I   K   V   I   S   K

        1450            1460            1470            1480            1490            1500            1510
          |               |               |               |               |               |               |
ATGACCCTAATAAGGATGATTACACGACTATACAGCAAACTGTGACAATGCAGACGACTATAAATGAGTATA
  Y   D   P   N   K   D   D   Y   T   T   I   Q   Q   T   V   T   M   Q   T   T   I   N   E   Y

        1520            1530            1540            1550            1560            1570            1580
          |               |               |               |               |               |               |
CTGGTGAGTTTAGAACAGCATCCTATGATAATACAATTGCTTTCTCTACAAGTTCAGGTCAAGGACAAGGTG
  T   G   E   F   R   T   A   S   Y   D   N   T   I   A   F   S   T   S   S   G   Q   G   Q   G

        1590            1600            1610            1620            1630            1640            1650
          |               |               |               |               |               |               |
ACTTGCCTCCTGAAAAAACTTATAAAATCGGAGATTACGTATGGGAAGATGTAGATAAAGATGGTATTCAAA
  D   L   P   P   E   K   T   Y   K   I   G   D   Y   V   W   E   D   V   D   K   D   G   I   Q

        1660            1670            1680            1690            1700            1710            1720
          |               |               |               |               |               |               |
ATACAAATGATAATGAAAAACCGCTTAGTAATGTATTGGTAACTTTGACGTATCCTGATGGAACTTCAAAAT
  N   T   N   D   N   E   K   P   L   S   N   V   L   V   T   L   T   Y   P   D   G   T   S   K

      1730            1740            1750            1760            1770            1780
        |               |               |               |               |               |
CAGTCAGAACAGATGAAGATGGGAAATATCAATTTGATGGGGTGCAGGTCGAC
  S   V   R   T   D   E   D   G   K   Y   Q   F   D   G   V   Q   V   D
                                                        ————————————————▶
                                                            Hyc tail
```

Sequence list. A partial nucleotide sequence of the putative *fig* gene from *S. epidermidis* strain HB and the deduced amino acid sequence. The vector sequences in the junction of the 5´- and 3´-ends are indicated.

Please add the following new paragraphs after the last line of text on page 21 of the application (i.e., at the end of the specification immediately before the claims):

--The nucleotide sequence shown in the above SEQ ID NO: 10 encodes a protein which contains 593 amino acids. SEQ ID NO: 11 is the amino acid sequence of this protein.

SEQ ID NO: 12 is the nucleotide sequence containing 1746 nitrogenous bases which code for the 582 amino acid FIG protein. As discussed above, the 582 amino acid FIG protein is encoded by the insert of pSE100. The nucleotide sequence of SEQ ID NO: 12 corresponds to bases 255-2000 shown in figures 6A-6E.

SEQ ID NO: 13 is the deduced amino acid sequence encoded by SEQ ID NO: 12. Thus SEQ ID NO: 13 is the 582 amino acid sequence of the FIG protein and thereby corresponds to amino acids 75-656 of the sequence depicted in figures 6A-6E. In other words SEQ ID NO: 13 is the amino acid sequence of SEQ ID NO: 11 without the Pel leader sequence and the Myc tail.

SEQ ID NO: 15 is the deduced amino acid sequence encoded by SEQ ID NO: 14, i.e., the amino acid sequence shown in figures 6A-6E.--